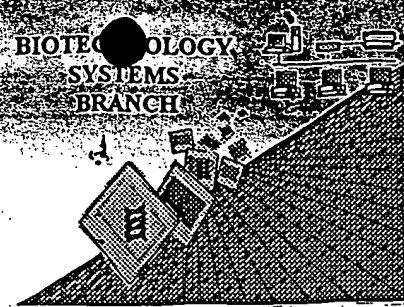# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09|897, 438A__

Source: __01 PC__

Date Processed by STIC: __11|14|01__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09|897, 438A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/897,438A TIME: 08:59:54

Input Set : A:\es.txt   **Does Not Comply**
Output Set: N:\CRF3\11142001\I897438A.raw **Corrected Diskette Needed**

```
 2 <110> APPLICANT: RIKEN
 4 <120> TITLE OF INVENTION: Reelin protein CR-50 epitope region
 6 <130> FILE REFERENCE: 04853.0076-00000
 8 <140> CURRENT APPLICATION NUMBER: US 09/897,438A
 9 <141> CURRENT FILING DATE: 2001-07-03
11 <150> PRIOR APPLICATION NUMBER: JP 2000-202801
12 <151> PRIOR FILING DATE: 2000-07-04
14 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
       56 <210> SEQ ID NO: 2
       57 <211> LENGTH: 117
       58 <212> TYPE: PRT
       59 <213> ORGANISM: Mus musculus
       61 <400> SEQUENCE: 2
       62 Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala Val Thr Phe Cys Glu
E--> 63 1               5                   10                      15
       65 Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys Leu Asn Thr Thr Thr
E--> 66         20                  25                      30
       68 Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe Ser
E--> 69         35                  40                      45
       71 Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr Ala
E--> 72     50                  55                      60
       74 Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser Thr
E--> 75 65                  70                      75                  80
       77 Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser Val
E--> 78             85                  90                      95
       80 Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr Glu
E--> 81         100                 105                     110
       83 Ala Cys Trp Ala Leu
       84         115
      174 <210> SEQ ID NO: 11
      175 <211> LENGTH: 18
      176 <212> TYPE: DNA
      177 <213> ORGANISM: Artificial Sequence
      179 <220> FEATURE:
      180 <223> OTHER INFORMATION: synthetic primer for PCR
      182 <400> SEQUENCE: 11
      183 gagcagtgtg gcaccatc                18
E--> 186
```

(1/7) delete

numbering is misaligned. See error summary sheet, item 3

VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: **US/09/897,438A**   TIME: 08:59:55

Input Set : **A:\es.txt**
Output Set: **N:\CRF3\11142001\I897438A.raw**

```
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:30 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:34 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:186 M:254 E: No. of Bases conflict, LENGTH:Input:7 Counted:19 SEQ:11
L:186 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:186 M:252 E: No. of Seq. differs, <211>LENGTH:Input:18 Found:19 SEQ:11
```